

Db	1120	GTGACTCTCTTTTCGATGATGTGTCACCAAGCTTCGACGACAAAGATTTGGAGTGGAG	1179
QY	908	acccttgatgaagtcgattgagcccaagctatagagctctggcgtgacaaagcaagatcccaatgag	967
Db	1180	ACCTTGACCCAGCTCCGTCGGGCCACGCTACCAAGCCCTGTGTGTCACAGGCACATCCCATGAC	1239
QY	968	tttaacctagaaagagagcaagaagatctgcaagatatacattccctctcggcgaagaaatllt	1027
Db	1240	TTACCTACAGAGAGGCGGAGAGAGCAGCTCCAGCATATACATTCCTTTGGCGAAGGAGATTT	1299
QY	1028	tattaccagcgagccatlltttgaggaaaccccactcagctccttaacatcacccagaa	1087
Db	1300	TATTACCATGACACCATTTTTCGCGGAGAACCCACCTACAGCTCTCTTAAACATCACCCAGGAA	1359
QY	1088	tgctttaaagaatctctcaagatccaaabaaatgacatagaagcccaatgcatgatgag	1147
Db	1360	TGCTCAAAAGCATCCCTCAAGGACAGAAAGAAAGATAGATAGAACCCCAATGCATATATGAA	1419
QY	1148	agccatctaaagaagatcttctcttcaacaaaccacataaatttatccccgaatat	1207
Db	1420	AGCCATCTTAACAGATTTTCTCTTCAACAAACCTACTATAAATCTTATCCCCGCAATAC	1479
QY	1208	tgctcgatatacatataagacctacctgagatataaagcttgcacagatgctcttgagag	1267
Db	1480	TGCTGAGATTATATCATAGAGCTTACCTGGCGCATATTAAAGCTTGTCAAGATCTCTTGGCAG	1539
QY	1268	acgaagaagatataatgattgattaaanaataagcttga	1303
Db	1540	ACCAAAACGATATATGTGCTTAAATAATTAATGTCTGCA	1575

	RESULT	2	PAT	29-SEP-1999
	AR066334			
	LOCUS	AR066334	182b bp	DNA
	DEFINITION	Sequence 8 from patent US 5849991.		
	ACCESSION	AR066334		
	VERSION	AR066334.1	GI:5966550	
	KEYWORDS			
	SOURCE	Unknown.		
	ORGANISM	Unknown.		
REFERENCE		Unclassified.		
AUTHORS		1 (bases 1 to 182b)		
TITLE		d'Ablice,A.J.F., Pearce,M.J., Rodins,A.J., Crawford,R.J. and Kallipen,P.D. Mice homozygous for an inactivated .alpha.1,3-galactosyl transferase gene Patent: US 5849991-A B 15-DEC-1998:		
JOURNAL		Location/Oalleiliars		
FEATURES		1..182b		
source		/organism "unknown"		
BASE COUNT		493 a 450 c 479 g 406 t		
ORIGIN				

Query Match	87.0%	Score 1133.6	DB 9	Length 1828
Best Local Similarity	95.4%	Pred. No. 1.5e-273		
Matches 1179	Conservative 0	Mismatches 54	Indels 3	Gaps 1

Qy	68	gsltllgaagaagctgaacattcgtctctcccaagccctgactctctctgtaaagaagac	127
Db	343	ggaactcgaagagctgcaaccttcgcttcccaacccctgcctctcttcttgagaaacgagc	402
Qy	128	lcaatagaacttgaatttgccttcttactctgaaagaaagaacgaatgaagaa	187
Db	403	tcacatgaacttctcttacttttgccttcttactctgaagaaagaaagcagacatgaagac	462
Qy	186	aaatataatgaatctcaagaagaaatgattctgccaatgctggttgcctcacaatgcat	247
Db	463	aaaataatgaatctcaagaagaaatgattctgccaatgctggttgcctcacaatgcat	522
Qy	248	gttggtgttttgagatataatcccaagcccaagaagccttctgtctgaatcaaacctatca	307
Db	523	gttggtgttttgagatataatcccaagcccaagaagccttctgtctgaatcaaacctatca	582

QY	308	adgaaccccaaaagtcagatggcgagagacagatcgaagaagatgagatgtttcccaattg	361
Db	583	AGAAACCCAGAGT---TGGTGGCAGCAGCATTCAGAAAGGCGCTGGTGGCTTCCACAAATGG	639
QY	368	tttaacatgattaccagaagaagaatgaagacgtaacgaadaaagaagaacgaagaag	427
Db	640	TTTAAACAATGTTTACCATGAGAGGATGAGACATATACCAATACAAAGCAAAATAAATAAAT	699
QY	428	gaagacaaagaagaagcttaaaatgataagacatgatcgaacgaatttaacgctgaagat	487
Db	700	GAAAGCAAGAAAGCAAGCTTAAACTATCCAGCTGGTTCAACCAATATTAACGCTCCAGAGTT	759
QY	488	gtagctatgagaagatgaaagacccctgctatggagaagacgttaccacgaagacgtctc	547
Db	760	CTGACATGACGAAGTGGAAAGCTCCAGTGGTGGGAAGGCACTTACACAAAGACCTGTC	819
QY	548	ltaagagattactacgcgaacgagaagaattacgctcgaagctgaagatcttcgagatcga	607
Db	820	TTAGACAAATATTATGCGAACCAAGAAATTAACCGTGGCGCGAGAGCTTTTCCGCTGGGA	879
QY	608	agatacatgaagcatctactggagaagatcttlaagctctgctaatgaagcctctgagat	667
Db	880	AGATACATTTAGCATTACCTTTAGAGAGCTTTACAGTCTCTATATAGCAATTCATGGTC	939
QY	668	ggcgaacgagacatcttllagctgaagatgaagacgtctccgaagatgctctgaagag	727
Db	940	GCCCAACCAGATCATCTTTATATATAGGTAAATGATGCTGTATAGATGCTTTCATATAGC	999
QY	728	ctgagcctctgctgctcttcaagatgattgaagtcgaagctgagaagagatgaacagac	787
Db	1000	TTGGGCTCTGCGCTCCTTAAAGTGTTTAAGTCAAGCCTCAGAGAAATGCGAGAGC	1055
QY	788	gtcagcatgagtagcaatgaagaacatcngagaagacatgtagctgacatccgagatgag	847
Db	1060	ATCCAGCATGATGGCATGAGAAATATGGGGAGATACATTCGAGTCATATCATATGAG	1111
QY	848	gtlgaatctccctctctgcatgagatgagacgaatcttccaaagagatctcgagatgag	907
Db	1120	CTGACCTCTCTTCTTGATGGAATGTCGACAGAGTCTCCAAAGCAAGTTCGAGTGGAG	1177
QY	908	acctcgaatgagtcgaatgagcccaatcacagcctgagtgaatacgaagagatcccgatgag	967
Db	1180	ACCGTGGCGAGTGGTGGTGGCCACTTAAAGCGTGGTGGTCAAGGTACATTCCTAAATGAG	1245
QY	968	tttacctacagaagaagcgaagaagatctcgacatagatctcccttcgagcgaagaagattt	1021
Db	1240	TTCACTTACGAGAGCGGAAGAGATCTGCACATACATTCCTTTGAGCAAGGAGATTTT	1291
QY	1028	tattacacgaagacatcttgaagagaacccacatgaagcttlaacatcacccaaaga	1081
Db	1300	TATTACATGCAAGCCATTTTGGGGGAACACCCAGCTAGGCTCTTACATCACCCAGGAA	1351
QY	1088	tgcttcaagaagatccttcaagacgaadaaatagacataagaagcccaatgaatgag	1141
Db	1360	TGCTTCAAGAGAAATCCTCAAGCAGCAAGAAATATACATACAGAGCCCATGGCTGATGAA	1411
QY	1148	agccatctaaccaagatcttcttcttaacgaacccctlaaactctataccctgagatc	1201
Db	1420	AGCCATCTTAAACAGATATTCTCTTCACACAAACCTACTAAATCTTATCTCCGGAATAC	1471
QY	1208	tactgagatattctataagcctacgtcgagatattaaatcttcaagatgcttgcagac	1261
Db	1480	TGCTGGGATTTATCATATAGGCTTACCTGGGATATTTAAGCTTGCAAGATGCTCTGGGTAG	1531
QY	1268	acnaaagaatataatgtagttaaaaataacgtctga	1303
Db	1540	ACAAACAGTATATATGTGTATCAATAATATCTCTGA	1575

RESULT 3

AF221508

AF221508

3684 bp

mRNA

MM

04 - FEB - 2001

[illegible]

RESULT	7
A69344	
LOCUS	A69344 1128 bp DNA PAT 06-MAY-1999
DEFINITION	Sequence 1 from patent WO9802453.
ACCESSION	A69344
VERSION	A69344.1 GI:4760171
KEYWORDS	'
SOURCE	unidentified.
ORGANISM	unidentified.
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 1128)
TITLE	Goudet, P., Robbrecht, P., Vandemeers, A. and Woelbroek, M. PEPTIDIC LIGANDS HAVING A HIGHER SELECTIVITY FOR THE V1RL RECEPTOR PATENT FOR THE VIP2 RECEPTOR Patent: WO 9802453-A 1 22-JAN-1998;
JOURNAL	UNIV BRUXELLES (BE) Location/Qualifiers
FEATURES	1..1128
source	/organism="unidentified" /db_xref="taxon:32644"
CDS	<1..1128 /note "unnamed protein product" /codon_start=1 /protein_id="CA342480.1" /db_xref="GI:4760172"
	//translation= NSKIMNKKGVVLSMLVSVYVYVFMYINSFQSLFWLYSKKN PVGSSAQRCWMPFSMFNCTHSTHEEDLAGNEURKRNCHLPLVWFNFGRER EVVITFMKAPVVEGVIYNRAVLNNYAKOILTVGLTAVAGRTIEYLDEFLSANI YEMGHKVIFYIWDOLISRMPL ELGLGRSRKFVFI KSEKMAQI SMSRMT IGDHII AHIDHEFLCMEVDVDFVORNFGCVETLDQSVALOMAWKKAHQELEYEKRSAAVY IFPGDGFYNAALFEGTPIYOVLNI TDCFGILIOLEENILFAWHIDESHINKFTLLN KPKILSLSEYCWYDHIGMSVDIRIKVKIAWKQKEYNLVANNI"
BASE COUNT	335 a 236 c 286 g 271 t
ORIGIN	

Query Match	Score	856.6	6	DB %	Length	1128
Best Local Similarity	87.0%					
Matches	982	Conservative	0	Mismatches	129	Indels
					18	Gaps
QY 187	qaaataatgaatctcaaggaaadgaatctatctgcatgctgatttctctcgaatctat	246				
DB 6	GAATAATATGATGTCCAAAGSAGACAGTGTCTGTCAATGTCGGTCTTCACATGTAT	65				
QY 247	tcctgctcttcgggaatatatccaaagccccaagaaqcccttttctctgataaacccatc	306				
DB 66	GCTTGTCTGTTGGCAATATACATCAACAGCCCGCAAGGTCTCTTGTTCGATATACCGTC	125				
QY 307	aagaaaccccaaaatcagtcgacgacgaagaatctcaaaagacatgattgatttcgaatg	466				
DB 126	AAAAAACCCACAGACT-----TGCCAGAGAGTGCTCAAGGGCCCTGGTGGTTCGAGCTTG	179				
QY 367	gttlaacatg-----gttcccaagaagaatgaagaagctgaagacgtgaagaaagaaga	417				
DB 180	GTTTACATATGGCATCTACACTTACCGAGGAAGAGAACGCTTATACGCTAACCAAAAGCA	239				
QY 418	acaaagaaagaaagaaacaa--aaagcaacgttlaagctatctgaactgattcaactcttaa	474				
DB 240	ACAAAGAAAGCAAGCAACGACAGAGAGACTGCCACTAGTGCAGCTGGTTATATCTCGAAG	209				
QY 475	aacgcccctgaagctctgaactatgaacatcttgaagaaagcaacccgagatgaggaagctta	544				
DB 300	ACGCCACAGAGCGTGGTACCATTACCAATACCAAGAGCTCCCAATGGTATGGAAGGCACTTA	359				
QY 535	caaaagagacgctcttlaagacgcttactacgccaagacagaaatgaactgagcctgaact	594				
DB 360	CAACAGAGCCGCTTTAGATAATTATTATGCCCAACAGAAAAATTATGCTGGGCTTGACAGCT	419				
QY 595	ttctgccttcggaagatatacatctgaacatctactggaagaattctctaacgtctctatga	654				
DB 420	TCTTGCCTGTGCAAGATATATTGAGCATATTCTGGAGAGAGTCTCTTAATATCTGTAATAC	479				
QY 655	qcaacttcaagcttgaagccgaagcttcaacttcttlaagctcatgattgaagaattctccagat	714				

[illegible][illegible]

	DB	960	CATCAGTCTACGAGAGTGCTTCACAGCGAATCTCCACBACAGCAAGAATAATGCATTACGAAGCCGCA	959
	Gy	1135	atgcaatgaagaaacatacttcaaacagaattttccttcacacaaccacttaaatct	1194
	Db	960	GTGGCATGATGAAGAACCAACTTAACAATGATTTCTGCTTCACAAACAACCCTAAATGTT	1019
	Gy	1195	atccccgaatctactgttggaattatcatatggcgctacctgcgaatatgaagtctttaa	1254
	Db	1020	ATCCGTAAGAAATAGCTGCTGGCATATCAATATAGGCAATGCTGTGGATATTAGCATTTGCCAA	1079
	Gy	1255	gatgtctggcacacaaaagattatattgttgttagaaataacacgtcga	1303
	Db	1080	CATACCTTGGCACAAAACAGATATATTGCTTTAGAAATATACATCTCCA	1128
Result	Y	571334	alpha 1,3 galactosyltransferase [New World monkeys, marmoset lymphoid cell line B95.8, mRNA Partial, 1141 nt].	
Accession		571334		
Version		S71333.1	GI:558051	
Keywords		New World monkeys.		
Source		Platyrrhini		
Organism		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates.		
Reference		1. (bases 1 to 1141)		
Authors		Hendon, T.R., Macher, H.A., Anuragi, F. and Gallili, D.		
Title		Defining the minimal size of catalytically active primate alpha 1,3 galactosyltransferase: structure-function studies on the recombinant truncated enzyme		
J-ORNL		Glycobiology 4 (2), 194-201 (1994)		
Medline		94131837		
Remark		GenBank staff at the National Library of Medicine created this entry [MBL accession I50270] from the original journal article. This sequence comes from Fig. 1.		
Features		location/qualifiers		
Source		1..1131		
		/organism="Platyrrhini"		
		/db_xref="taxon:9479"		
		/cell_line="lymphoid cell line B95.8"		
		1..1131		
		/note="This sequence comes from Fig. 1: conceptual translation differs from the translation presented in the manuscript (251ty>251): alpha 1,36T"		
		/codon_start=1		
		/product="alpha 1,3 galactosyltransferase"		
		/protein_id="AAH1587.2"		
		/db_xref="GI:7717225"		
		/translation="MNRKGVILSLVSTVIYFMEYINSFGSLFIYHSRNPVEDDSSQKRWMPREGNNINHYVCEDEEDDKERGEFPKKEDDTETLRIMDFPKRRPEWVTIQMKAPVWVEGIVNKALIENTYAOKITVGITVAIGYISHTVIREVTSANRYHPVGRKVLFEYWDVDVSRAPELEGLPSKFVFEFKPKRMODISMKRKTIGEHIALHIVGGKPLFCMDVDVQDPDRPGEVLIQSVAQLQAWMYRKADPDFTYERKESAAVTPRGSGDEVYHAALPGSTPIOVNLTIOECPKGILLIKNDIDIAEMHDESINKYFLLNKSEKLSPEVCWHYHGCTGPSDKIFVLSMOTKEYNLVRKNV"		
BASE COUNT		345 a 224 c 283 g 280 t		
ORIGIN				
Query Match		61.9%; Score 806.8; DB 97; Length 1131;		
Fast Local Similarity		84.2%; Pred. No. 1,36-194;		
Matches		955; Conservative 0; Mismatches 152; Indels 27; Gaps 3;		
Gy	194	atgcaatgaagaaacatacttctgcacatctgtgtgtctcaactgtcattgtgtg	253	
Db	1	ATGCAATGCAAGGCAAAATATATCTTCGCAAGTGTGTTGTCACAACTGATTTCTTG	60	
Gy	254	ttttggaattatctccacagatcccgaagaagcttltgtctcgaataaccatccaagaac	313	
Db	61	TTTTGGCAATATATTAACAGGTCACAAGGCTCTTCTTGCGATATATACCTGCAAGAAC	120	

[illegible]

[illegible][illegible]

QY 895 gttccagatggaagccggaagatgagttggtccagctacagcgtctgtgtacaaagc 954
DB 684 ctttgagggtggagacccctggccgacgtgcgtgagctaacagccgtgtgtacaaagc 743
QY 955 atatacctcaatgaatcttactacagagagagagatctgacagatcttcccttcgg 1014
DB 744 acatctctgacagagcttactacagagagagagatctgacagatcttcccttcgg 803
QY 1015 ggaagagagatcttactacagagagagatcttctgagagagagagagagagagag 1074
DB 804 ccagagagagatcttactacagagagagagatcttctgagagagagagagagagag 863
QY 1075 gttccagatggaagccggaagatgagttggtccagctacagcgtctgtgtacaaagc 1134
DB 864 ctttgagggtggagacccctggccgacgtgcgtgagctaacagccgtgtgtacaaagc 923
QY 1135 atgagctgag 1194
DB 924 gttccagatggaagccggaagatgagttggtccagctacagcgtctgtgtacaaagc 983
QY 1195 atgagctgag 1254
DB 984 atgagctgag 1043
QY 1255 atgagctgag 1303
DB 1044 gatagctgag 1092

RESULT 14
A69348
LOCUS A69348 1065 bp DNA PAT 06-MAY-1999
DEFINITION Sequence 5 from Patent WO9802453.
ACCESSION A69348
VERSION A69348.1 GI:4760175
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1065)
AUTHORS Goulet, P., Robberts, P., Vandermeers, A. and Woelbroeck, M.
TITLE PEPTIDE LIGANDS HAVING A HIGHER SELECTIVITY FOR THE VIP1 RECEPTOR
JOURNAL THIN FOR THE VIP2 RECEPTOR
PATENT: WO 9802453-A 5 22-JAN-1998;
UNIV BRUXELLES (BE)
FEATURES
Location/Qualifiers
1..1065
CDS
/organism="unidentified"
/db_xref="taxon:32644"
/note="unnamed protein product"
/codon_start=1
/protein_id="CAH42482.1"
/db_xref="gi:4760176"
/translation="MSKIMNKGRVYVLSMLVSTYVYVMEYINSPELSFRTYQSKT
HSYAEEDAKIGNEKQKEDNKGELFLVDNENPEKRPVVIITRKAVVWEGTYNKA
VLNLYVAKGIIIVLTVLAVCYIERYLEPFLISANTYVWGHVIFVIMVDSIRNP
LELGLPKSFVKELSEKPMQDISMHRKLTGELIHLAIOHEVYVLFQCMVDQYFN
NGVETLCKSVKQIQAMMYKAPDEFTYERKESAYILEFGGDFYFAALHGGCTPTQ
VNTFOHDKGIIQKENDITAEHMDHSHLNKYLPLNNPKILSLFVYMDHIGMSVD
IRIVKINWKKRYNLYVRNT"

BASE COUNT 320 a 224 c 264 g 257 t
ORIGIN

Query Match 59.0%; Score 769.2; DB 9; Length 1065;
Best Local Similarity 82.9%; Pred. No. 3,4e-182;
Matches 929; Conservative 0; Mismatches 128; Indels 63; Gaps 2;

QY 187 gaaatadadgaatgctgaagaaagatgctgcaatgctggttctcgaacttcat 246
DB 6 GAAATAATGAAATGCTGAAGAAAGATGCTGCAATGCTGCTTCTCAACTGTAAT 65

QY 247 ttttgggttttgggaataatattccgaagccgaagagcttttgttgtgaatccatc 306
DB 66 gcttgtgttttggcaatgacatcaaacagccgaaggttttgttgtgaatgacatc 125
QY 307 aagaagccgaagatgctgagagagagatctgagagagagagagagagagagagagag 366
DB 126 AAGAGCTC----- 133
QY 367 gtttaacatgatttaccagaagagagatggaagagctgagagagagagagagagagag 426
DB 134 -----ACAGTTACCCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 185
QY 427 ggaag 484
DB 186 AG 245
QY 484 gtttgaacatgatttaccagaagagagatggaagagctgagagagagagagagagagag 543
DB 246 gtttgaacatgatttaccagaagagagatggaagagctgagagagagagagagagagag 605
QY 544 gtttgaacatgatttaccagaagagagatggaagagctgagagagagagagagagagag 603
DB 306 GCTGTACATTAATTTATGCAAAACAGAAATTAACCTTGCCCTTGAGAGATTTGAGTGT 465
QY 604 cgaagagatgatttaccagaagagagatggaagagctgagagagagagagagagagag 664
DB 306 CCGAGATACATTAAGAGATTAAGTGGAGAGCTTTTAATATGCTTAATTAATTAATTA 425
QY 664 gtttgaacatgatttaccagaagagagatggaagagctgagagagagagagagagagag 723
DB 426 GGTGGCCAGAAAGTCATCTTTTACATGATGATGATGATGATGATGATGATGATGAT 485
QY 724 agagctgag 783
DB 486 AGAGCTGGAGTCTCTGCGCTGCTTTAAAGTGTGAGATTAAGTGGAGAGCTTGA 545
QY 784 ggaag 843
DB 546 AGAGATACAGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 605
QY 844 tgaag 903
DB 606 CAGAGTGGAGTCTCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 665
QY 904 ggaag 963
DB 666 CAG 725
QY 964 tgaag 1023
DB 726 CAGAGTGGAGTCTCTGCGCTGCTTTAAAGTGTGAGATTAAGTGGAGAGCTTGA 785
QY 1024 ttttgaacatgatttaccagaagagagatggaagagctgagagagagagagagagagag 1083
DB 786 TTTTATTAACAG 845
QY 1084 ggaag 1143
DB 846 CAGAGTGGAGTCTCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 905
QY 1144 tgaag 1203
DB 906 TGAAG 965
QY 1204 atgag 1263
DB 966 ATAGCTGCTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1023
QY 1264 ggaag 1303
DB 1026 CAG 1065

•
•
•